

AMENDMENTS TO THE CLAIMS

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-13. (canceled)

14. (currently amended) A method for the production of L-amino acids using coryneform bacteria comprising:

- a) fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide comprises a nucleotide sequence of SEQ ID NO:1 ~~and encodes a polypeptide having an RNA polymerase sigma C factor activity~~ , wherein said overexpression is achieved by increasing the copy number of said polynucleotide or by operably linking said polynucleotide to a promoter.

15. (canceled)

16. (previously presented) The method according to claim 14, further comprising:
isolating the L-amino acid.

17. (previously presented) The method according to claim 14, wherein the L amino acid is lysine.

18. (currently amended) A method for the production of L-amino acids using coryneform bacteria comprising:

fermenting coryneform bacteria which produce a desired L-amino acid comprising an overexpressed polynucleotide sigC wherein said polynucleotide encodes a polypeptide comprising an amino acid sequence of SEQ ID NO:2, wherein said overexpression is achieved by increasing the copy number of said polynucleotide.

19-20. (canceled)

21. (currently amended) The method according to claim 14, wherein ~~a strain transformed with a plasmid vector is used, and the plasmid vector carries the nucleotide sequence coding for the sigC gene~~ increasing the copy number is achieved by transforming said coryneform bacteria with a vector comprising said polynucleotide.

22-24. (canceled)

25. (currently amended) The method according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are overexpressed; wherein the one or more genes is/are selected from the group consisting of:

a gene ~~dap~~A coding for dihydrodipicolinate synthase,

a gene ~~gap~~ coding for glyceraldehyde-3-phosphate dehydrogenase,

a gene ~~tpi~~ coding for triosephosphate isomerase,

a gene ~~pgk~~ coding for 3-phosphoglycerate kinase,

a gene ~~zwf~~ coding for glucose-6-phosphate dehydrogenase,
a gene ~~pye~~ coding for pyruvate carboxylase,
a gene ~~mqr~~ coding for malate-quinone-oxidoreductase,
a gene ~~lysC~~ coding for a ~~feedback-resistant~~ aspartate kinase,
~~gene lysE coding for a protein for lysine export,~~
a gene ~~hom~~ coding for homoserine dehydrogenase,
a gene ~~ilvA~~ coding for threonine dehydratase ~~or allele ilvA(Fbr) coding for a~~
~~feedback-resistant threonine dehydratase,~~
a gene ~~ilvBN~~ coding for acetohydroxy acid synthase,
a gene ~~ilvD~~ coding for dihydroxy acid dehydratase, and
a gene ~~zwa1~~ coding for ~~the~~ a Zwa1 protein.

26. (currently amended) Process according to claim 14, wherein the bacteria being fermented comprise, at the same time, one or more genes which are eliminated; wherein the genes are selected from the group consisting of:

a gene ~~pek~~ coding for phosphoenol pyruvate carboxykinase,
a gene ~~pgi~~ coding for glucose-6-phosphate isomerase,
a gene ~~poxB~~ coding for pyruvate oxidase, ~~and~~
~~gene zwa2 coding for the Zwa2 protein.~~

27. (previously presented) The method according to claim 14 wherein the bacteria is *Corynebacterium glutamicum*.

28. (currently amended) The method according to claim ~~21~~ 27, wherein ~~the Corynebacterium glutamicum is a~~ said vector is pEC-XK99EsigCb2ex contained in Escherichia coli strain of DH5 α mcr/pEC-XK99EsigCb2ex deposited under DSM 14375.
29. (currently amended) ~~The method according to claim 27, wherein the Corynebacterium~~ Corynebacterium glutamicum ~~is a strain of~~ DSM5715/pEC-XK99E deposited under DSM 13455.
- 30-32. (canceled)
33. (new) The method according to claim 18 wherein said polynucleotide comprises nucleotides 300 to 878 of SEQ ID:1.
34. (new) A method for the production of L-amino acids using coryneform bacteria comprising:
fermenting coryneform bacteria which produce a desired L-amino acid
comprising an overexpressed polynucleotide sigC wherein said polynucleotide
comprises a nucleotide sequence of SEQ ID NO:1 and encodes a polypeptide
having an RNA polymerase sigma-C factor.